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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/993,292B

DATE: 10/12/2004

TIME: 12:06:10

Input Set : A:\09-993,292 Sequence Listing.txt

Output Set: N:\CRF4\10122004\I993292B.raw

3 <110> APPLICANT: University of Maryland, Baltimore  
 4 GALEN, James E.  
 6 <120> TITLE OF INVENTION: USE OF CLYA HEMOLYSIN FOR EXCRETION OF PROTEINS  
 8 <130> FILE REFERENCE: A8461  
 10 <140> CURRENT APPLICATION NUMBER: 09/993,292B  
 11 <141> CURRENT FILING DATE: 2001-11-23  
 13 <150> PRIOR APPLICATION NUMBER: US 60/252,516  
 14 <151> PRIOR FILING DATE: 2000-11-22  
 16 <160> NUMBER OF SEQ ID NOS: 28  
 18 <170> SOFTWARE: PatentIn version 3.3  
 20 <210> SEQ ID NO: 1  
 21 <211> LENGTH: 6271  
 22 <212> TYPE: DNA  
 23 <213> ORGANISM: Artificial Sequence  
 25 <220> FEATURE:  
 26 <223> OTHER INFORMATION: pSEC84 Expression Plasmid  
 28 <400> SEQUENCE: 1

ENTERED

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33	taaagttaat	gatgatagcg	ggagttattc	tagttgcgag	tgaaggtttt	gttttgacat	180
35	tcagtgtctg	caaatactta	agaataagtt	attgatttta	accttgaatt	attattgctt	240
37	gatgttaggt	gcttatttcg	ccattccgca	ataatcttaa	aaagttccct	tgcatttaca	300
39	ttttgaaaca	tctatagcga	taaatgaaac	atcttaaaaag	ttttagttatc	atattcgtgt	360
41	tggattattc	tgcatttttg	gggagaatgg	acttgccgac	tgattaatga	gggttaatca	420
43	gtatgcagt	gcataaaaaa	gcaaataaag	gcatataaca	gatcgatctt	aaacatccac	480
45	aggaggatgg	gatccaaaat	aaggaggaaa	aaaaaatgac	tagtattttt	gcagaacaaa	540
47	ctgtagaggt	agttaaaagc	gcgatcgaaa	ccgcagatgg	ggcattagat	ctttataaca	600
49	aatacctcga	ccaggtcatc	ccctggaaga	cctttgatga	aaccataaaa	gagttaagcc	660
51	gttttaaaaca	ggagtactcg	caggaagctt	ctgttttagt	tggtgatatt	aaagttttgc	720
53	ttatggacag	ccaggacaag	tattttgaag	cgacacaaac	tgtttatgaa	tggtgtggtg	780
55	tcgtgacgca	attactctca	gcgtatattt	tactatttga	tgaatataat	gagaaaaaag	840
57	catcagccca	gaaagacatt	ctcattagga	tattagatga	tggtgtcaag	aaactgaatg	900
59	aagcgcaaaa	atctctcctg	acaagttcac	aaagtttcaa	caacgcttcc	ggaaaaactgc	960
61	tggcattaga	tagccagtta	actaatgatt	tttcggaaaa	aagtagttat	ttccagtcac	1020
63	aggtggatag	aattcgtaag	gaagcttatg	ccggtgctgc	agccggcata	gtcgcgggtc	1080
65	cgtttggtg	aattatttcc	tattctattg	ctgcgggcgt	gattgaagg	aaattgattc	1140
67	cagaattgaa	taacaggcta	aaaacagtgc	aaaatttctt	tactagctta	tcagctacag	1200
69	tgaacaagc	gaataaagat	atcgatgcgg	caaaattgaa	attagccact	gaaatagcag	1260
71	caattgggga	gataaaaacg	gaaaccgaaa	caaccagatt	ctacgttgat	tatgatgatt	1320
73	taatgctttc	tttattaaaa	ggagctgcaa	agaaaatgat	taacacctgt	aatgaatacc	1380
75	aacaacgtca	tggtagaag	acgcttttcg	aggttccctga	cgtcgctagc	tgataaccta	1440
77	gggccagcaa	aaggccagga	accgtaaaaa	ggccgcgttg	ctggcggttt	tccataggct	1500
79	ccgccccctt	gacgagcatc	acaaaaatcg	acgctcaagt	cagaggtggc	gaaaccgcag	1560

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81	aggactataa	agataccagg	cgtttccccc	tggaagctcc	ctcgtgcgct	ctcctgttcc	1620
83	gaccctgcgc	cttaccggat	acctgtccgc	ctttctccct	tccggaagcg	tggcgctttc	1680
85	tcatagctca	cgctgtaggt	atctcagttc	ggtgtaggtc	gttcgctcca	agctgggctg	1740
87	tgtgcacgaa	cccccggtc	agcccgaccg	ctgcgcctta	tccggttaact	atcgtcttga	1800
89	gtccaacccg	gtaagacacg	acttatcgcc	actggcagca	gccactggta	acaggattag	1860
91	cagagcgagg	tatgtaggcg	gtgctacaga	gttcttgaag	tggtggccta	actacggcta	1920
93	cactagaagg	acagtatttg	gtatctgcgc	tctgctgaag	ccagttacct	tcggaaaaag	1980
95	agttggtagc	tcttgatccg	gcaaacaaac	caccgctggg	agcgggtggt	tttttgtttg	2040
97	caagcagcag	attacgcgca	gaaaaaaaag	atctcaagaa	gatcctttga	tcttttctac	2100
99	ggggtctgac	gctcagtaga	tctaaaacac	taggccccag	agttttaga	aacgcaaaaa	2160
101	ggccatccgt	caggatggcc	ttctgcttaa	tttgatgcct	ggcagtttat	ggcgggcgtc	2220
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105	tctactcag	gagagcgttc	accgacaaac	aacagataaa	acgaaaggcc	cagtctttcg	2340
107	actgagcctt	tcgttttatt	tgatgcctgg	cagttcccta	ctctcgcatg	gggagacccc	2400
109	acactaccat	cggcgctacg	gcgtttcact	tctgagttcg	gcatggggtc	aggtgggacc	2460
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113	atctgtatca	ggctgaaaat	cttctctcat	ccgccaaaac	agccaagctg	gatctggcaa	2580
115	atcgctgaat	attccttttg	tctccgacca	tcaggcacct	gagtcgctgt	ctttttcgtg	2640
117	acattcagtt	cgctgcgctc	acggctctgg	cagtgaatgg	gggtaaaatg	cactacaggc	2700
119	gccttttatg	gattcatgca	aggaaactac	ccataatata	agaaaagccc	gtcacgggct	2760
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125	agactggcta	atgcacccag	taaggcagcg	gtatcatcaa	caggcttacc	cgtcttactg	2940
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135	gccaacgcta	tgtcctgata	gcggtccgcc	acaccagccc	ggccacagtc	gatgaatcca	3240
137	gaaaagcggc	cattttccac	catgatattc	ggcaagcagg	catcgccatg	ggtcacgacg	3300
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153	cgcctcgtcg	ctgacagcgg	gaacacggcg	gcacagagc	agccgattgt	ctgttggtgc	3780
155	cagtcatagc	cgaatagcct	ctccacccaa	gcggccggag	aacctgcgtg	caatccatct	3840
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171	cttcgtggta	gtttcatggc	cttcttctcc	ttgcgcaaag	cgcggtaaga	ggctatcctg	4320
173	atgtggacta	gacataggga	tgctcgtggg	tggttaatga	aaattaactt	actacggggc	4380
175	tatcttcttt	ctgccacaca	acacggcaac	aaaccacctt	cacgtcatga	ggcagaaagc	4440
177	ctcaagcgcc	gggcacatca	tagcccatat	acctgcacgc	tgaccacact	cactttccct	4500

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179 gaaaataatc cgctcattca gaccgttcac gggaaatccg tgtgattgtt gccgcatcac 4560
181 gctgcctccc ggagtttgtc tcgagcactt ttgttaccgc ccaaacaaaa cccaaaaaca 4620
183 acccataccc aaccaataa aacacccaaa caagacaaat aatcattgat tgatggttga 4680
185 aatggggtaa acttgacaaa caaacccact taaaacccaa aacataccca aacacacacc 4740
187 aaaaaaacac cataaggagt ttataaatg ttggtattca ttgatgacgg ttcaacaaac 4800
189 atcaaactac agtggcagga aagcgacgga acaattaaac agcacattag cccgaacagc 4860
191 ttcaaacgcg agtgggcagt ctcttttggg gataaaaagg tctttaacta cacactgaac 4920
193 ggcgaaacagt attcatttga tccaatcagc cgggatgctg tagtcacaac caatatcgca 4980
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240 &lt;210&gt; SEQ ID NO: 2

241 &lt;211&gt; LENGTH: 305

242 &lt;212&gt; TYPE: PRT

243 &lt;213&gt; ORGANISM: Salmonella typhi

245 &lt;400&gt; SEQUENCE: 2

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247 Met Thr Ser Ile Phe Ala Glu Gln Thr Val Glu Val Val Lys Ser Ala
248 1 5 10 15
251 Ile Glu Thr Ala Asp Gly Ala Leu Asp Leu Tyr Asn Lys Tyr Leu Asp
252 20 25 30
255 Gln Val Ile Pro Trp Lys Thr Phe Asp Glu Thr Ile Lys Glu Leu Ser
256 35 40 45
259 Arg Phe Lys Gln Glu Tyr Ser Gln Glu Ala Ser Val Leu Val Gly Asp
260 50 55 60
263 Ile Lys Val Leu Leu Met Asp Ser Gln Asp Lys Tyr Phe Glu Ala Thr
264 65 70 75 80
267 Gln Thr Val Tyr Glu Trp Cys Gly Val Val Thr Gln Leu Leu Ser Ala
268 85 90 95
271 Tyr Ile Leu Leu Phe Asp Glu Tyr Asn Glu Lys Lys Ala Ser Ala Gln
272 100 105 110
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275 Lys Asp Ile Leu Ile Arg Ile Leu Asp Asp Gly Val Lys Lys Leu Asn
276      115      120      125
279 Glu Ala Gln Lys Ser Leu Leu Thr Ser Ser Gln Ser Phe Asn Asn Ala
280      130      135      140
283 Ser Gly Lys Leu Leu Ala Leu Asp Ser Gln Leu Thr Asn Asp Phe Ser
284 145      150      155      160
287 Glu Lys Ser Ser Tyr Phe Gln Ser Gln Val Asp Arg Ile Arg Lys Glu
288      165      170      175
291 Ala Tyr Ala Gly Ala Ala Ala Gly Ile Val Ala Gly Pro Phe Gly Leu
292      180      185      190
295 Ile Ile Ser Tyr Ser Ile Ala Ala Gly Val Ile Glu Gly Lys Leu Ile
296      195      200      205
299 Pro Glu Leu Asn Asn Arg Leu Lys Thr Val Gln Asn Phe Phe Thr Ser
300      210      215      220
303 Leu Ser Ala Thr Val Lys Gln Ala Asn Lys Asp Ile Asp Ala Ala Lys
304 225      230      235      240
307 Leu Lys Leu Ala Thr Glu Ile Ala Ala Ile Gly Glu Ile Lys Thr Glu
308      245      250      255
311 Thr Glu Thr Thr Arg Phe Tyr Val Asp Tyr Asp Asp Leu Met Leu Ser
312      260      265      270
315 Leu Leu Lys Gly Ala Ala Lys Lys Met Ile Asn Thr Cys Asn Glu Tyr
316      275      280      285
319 Gln Gln Arg His Gly Lys Lys Thr Leu Phe Glu Val Pro Asp Val Ala
320      290      295      300

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323 Ser

324 305

327 <210> SEQ ID NO: 3

328 <211> LENGTH: 102

329 <212> TYPE: DNA

330 <213> ORGANISM: Artificial Sequence

332 <220> FEATURE:

333 <223> OTHER INFORMATION: Cloning Primer

335 <400> SEQUENCE: 3

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338 tagttaaaag cgcgatcgaa accgcagatg gggcattaga tc 102

341 <210> SEQ ID NO: 4

342 <211> LENGTH: 101

343 <212> TYPE: DNA

344 <213> ORGANISM: Artificial Sequence

346 <220> FEATURE:

347 <223> OTHER INFORMATION: Cloning Primer

349 <400> SEQUENCE: 4

350 cctaggttat cagctagcga cgtcaggaac ctcgaaaagc gtcttcttac catgacgttg 60

352 ttggtattca ttacaggtgt taatcatttt ctttgcagct c 101

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356 <211> LENGTH: 97

357 <212> TYPE: DNA

358 <213> ORGANISM: Artificial Sequence

360 <220> FEATURE:

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361 <223> OTHER INFORMATION: Cloning Primer
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366 tagacagctt atcatcgata agctttaatg cggtagt                                97
369 <210> SEQ ID NO: 6
370 <211> LENGTH: 69
371 <212> TYPE: DNA
372 <213> ORGANISM: Artificial Sequence
374 <220> FEATURE:
375 <223> OTHER INFORMATION: Cloning Primer
377 <400> SEQUENCE: 6
378 agatctacta gtgtcgacgc tagctatcag gtcgaggtgg cccggctcca tgcaccgcga      60
380 cgcaacgcg                                                                69
383 <210> SEQ ID NO: 7
384 <211> LENGTH: 60
385 <212> TYPE: DNA
386 <213> ORGANISM: Artificial Sequence
388 <220> FEATURE:
389 <223> OTHER INFORMATION: Cloning Primer
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396 <211> LENGTH: 101
397 <212> TYPE: DNA
398 <213> ORGANISM: Artificial Sequence
400 <220> FEATURE:
401 <223> OTHER INFORMATION: Cloning Primer
403 <400> SEQUENCE: 8
404 cattaaagggt tatcgatgat aagctgtcaa acatgagcta gcctagggtca ttaccaatgc      60
406 ttaatcagtg aggcacctat ctcagcgatc tgtctatttc g                                101
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410 <211> LENGTH: 101
411 <212> TYPE: DNA
412 <213> ORGANISM: Artificial Sequence
414 <220> FEATURE:
415 <223> OTHER INFORMATION: Cloning Primer
417 <400> SEQUENCE: 9
418 cgaaatagac agatcgctga gataggtgcc tctactgatta agcattggta atgacctagg      60
420 ctagctcatg tttgacagct tatcatcgat aacctttaat g                                101
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424 <211> LENGTH: 71
425 <212> TYPE: DNA
426 <213> ORGANISM: Artificial Sequence
428 <220> FEATURE:
429 <223> OTHER INFORMATION: Cloning Primer
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432 gcgcactagt aaagaaacga accaaaagcc atataaggaa acatacggca tttcccatat      60
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437 <210> SEQ ID NO: 11

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**VERIFICATION SUMMARY**

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